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Dwarf) coconut palm. Figure 10B shows the high number of polymorphous DNA fragments visible by gel analysis with a single ISTR primer combination. Figure 10C shows 30 of these bands analyzed using known methods of cluster analysis to obtain phenograms according to the UPGMA method (SAHN-clustering)and by PCA (principal coordinate analysis).

IN THE CLAIMS:

Please cancel claims 12-15 without prejudice or disclaimer of the subject matter contained therein.

Please amend the claims as follows:

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2. (Amended) A method for performing DNA-fingerprint analysis using a primer or primer pair comprising:

(e) providing genomic DNA sequences from different species, wherein said DNA sequences encode an endonuclease, a reverse transcriptase or a RNAse H of a copia or copia-like element and wherein said DNA sequences are of animal, plant, human, prokaryotic or eukaryotic origin;

(f) subjecting said DNA sequences to a PCR reaction with a primer or primer pair, wherein said primer or primer pair hybridizes to said DNA sequences;

(g) separating the PCR products and;

(h) determining the degree of genetic relatedness between the DNA sequences.

2. (Amended) The method according to claim 1, wherein the DNAs sequences are derived from:

(a) the animal kingdom with all its subkingdoms, phylums, subphylums, families, genus and species;

(b) the plant kingdom with all its subkingdoms, phylums, subphylums, families, genus and species;

(c) humans; and

(d) microorganisms comprising prokaryotic microorganisms and eukaryotic microorganisms.

3. (Amended) The method according to claim 1, wherein the DNAs to be analyzed are separated on a gel according to the length of the PCR products.

8. (Amended) The method according to claim 3, wherein the gel is a sequencing gel.

9. (Amended) The method according to claim 3 or 4, further comprising the steps of performing a Southern blot and transferring the DNAs onto a membrane whereby hybridization can be visualized with a probe.

10. (Amended) The method according to claim 5, wherein the probe is the primer or the primer pair hybridizes to said DNA sequences.

11. (Amended) The method according to claim 1, wherein the primer or primer pair is labeled.

11. (Amended) The method according to claim 7, wherein the label is a non-radioactive label, biotin, a fluorescence dye, a dye or a radioactive label.

12. (Amended) The method according to any one of claims 1 to 8, wherein the primer or primer pair corresponds to any one of the sequences selected from the group consisting of SEQ ID NOS 4-45.

13. (Amended) The method according to claim 1, wherein the primer or primer pair comprises a sequence which overlaps with any one of the sequences selected from the group consisting of SEQ ID NOS 4-45.

14. (Amended) The method according to claim 1, wherein the fingerprint analysis is used for studying biodiversity, genetic relationship, taxonomy.

Please add the following new claims:

15. (New) The method according to claim 8, wherein the non-radioactive label is digoxigenin.

16. (New) The method according to claim 8, wherein the radioactive label is 75^{32} P.

14. (New) The method according to claim 2, wherein the DNAs sequences are derived from gram-positive or gram-negative bacteria.

15. (New) The method according to claim 2, wherein the DNAs sequences are derived from the class of Dicotyledonae.

16. (New) The method according to claim 2, wherein the DNAs sequences are derived from fungi or ascomycetes.

17. (New) The method according to claim 2, wherein the DNAs sequences are derived from the family of hominids or the family of Bovidae.

18. (New) The method according to claim 2, wherein the DNAs sequences are derived from the class of Monocotyledonae.